SEQUENCE LISTING

<110> Meyers, Rachel A.
      MacBeth, Kyle J.

<120> 14094, A NOVEL TRYPSIN FAMILY MEMBER AND
   USES THEREFOR

<130> 10448-046002

<150> US 09/633,300
<151> 2000-08-08

<150> US 60/200,621
<151> 2000-04-28

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 2948
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (628)...(1986)

<221> misc_feature
<222> (1)...(2948)
<223> n = A,T,C or G

<400> 1
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aagagttgca tatcgcctcc catcaacaaa ctttccntgt atttccanac aatgtatttt      60
gtttgtcaaa tccagttttc ttgtaaacat tggggggtaa ataacagagg tggcttatga     120
gtatttcttc cagggtaaaa agcaaaagaa ttccggtttt ctgtatcctt ttcacttact     180
gttacccact ttgcctcgtc ttcaccctgt ccaaacaccg gtctccaatt tgcccttcag     240
agaacttaag tcaaggagag ttgaaattca caggccaggg cacatctttt atttatttca     300
ttatgttggc caacagaact tgattgtaaa taataataaa gaaatctgtt atatactttc     360
caaactccaa aaaaaaaccg gaattcagcc tggttaagtc caagctgaat tccgggtggg     420
ggaaggaccg ggcaccggac ggctcgggta ctttcgttct taattaggtc atgcccgtat     480
gagccaggaa agggctgtgt ttatgggaag ccagtaacac tgtggcctac tatctcttcc     540
gtggtgccat ctacattttt gggactcggg aattatgagg tagaggtgga ggcggagccg     600
gatgtcagag gtcctgaaat agtcacc atg ggg gaa aat gat ccg cct gct gtt     654
                                Met Gly Glu Asn Asp Pro Pro Ala Val
                                 1               5
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gaa gcc ccc ttc tca ttc cga tcg ctt ttt ggc ctt gat gat ttg aaa     702
Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys
 10              15                  20                  25
```

```
ata agt cct gtt gca cca gat gca gat gct gtt gct gca cag atc ctg     750
Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu
            30                  35                  40
```

```
tca ctg ctg cca ttg aag ttt ttt cca atc atc gtc att ggg atc att        798
Ser Leu Leu Pro Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile
            45                  50                  55

gca ttg ata tta gca ctg gcc att ggt ctg ggc atc cac ttc gac tgc        846
Ala Leu Ile Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys
        60                  65                  70

tca ggg aag tac aga tgt cgc tca tcc ttt aag tgt atc gag ctg ata        894
Ser Gly Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile
        75                  80                  85

gct cga tgt gac gga gtc tcg gat tgc aaa gac ggg gag gac gag tac        942
Ala Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr
90                  95                  100                 105

cgc tgt gtc cgg gtg ggt ggt cag aat gcc gtg ctc cag gtg ttc aca        990
Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe Thr
                110                 115                 120

gct gct tcg tgg aag acc atg tgc tcc gat gac tgg aag ggt cac tac       1038
Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly His Tyr
                125                 130                 135

gca aat gtt gcc tgt gcc caa ctg ggt ttc cca agc tat gtg agt tca       1086
Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr Val Ser Ser
                140                 145                 150

gat aac ctc aga gtg agc tcg ctg gag ggg cag ttc cgg gag gag ttt       1134
Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe Arg Glu Glu Phe
        155                 160                 165

gtg tcc atc gat cac ctc ttg cca gat gac aag gtg act gca tta cac       1182
Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys Val Thr Ala Leu His
170                 175                 180                 185

cac tca gta tat gtg agg gag gga tgt gcc tct ggc cac gtg gtt acc       1230
His Ser Val Tyr Val Arg Glu Gly Cys Ala Ser Gly His Val Val Thr
                190                 195                 200

ttg cag tgc aca gcc tgt ggt cat aga agg ggc tac agc tca cgc atc       1278
Leu Gln Cys Thr Ala Cys Gly His Arg Arg Gly Tyr Ser Ser Arg Ile
                205                 210                 215

gtg ggt gga aac atg tcc ttg ctc tcg cag tgg ccc tgg cag gcc agc       1326
Val Gly Gly Asn Met Ser Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser
        220                 225                 230

ctt cag ttc cag ggc tac cac ctg tgc ggg ggc tct gtc atc acg ccc       1374
Leu Gln Phe Gln Gly Tyr His Leu Cys Gly Gly Ser Val Ile Thr Pro
        235                 240                 245

ctg tgg atc atc act gct gca cac tgt gtt tat gac ttg tac ctc ccc       1422
Leu Trp Ile Ile Thr Ala Ala His Cys Val Tyr Asp Leu Tyr Leu Pro
250                 255                 260                 265

aag tca tgg acc atc cag gtg ggt cta gtt tcc ctg ttg gac aat cca       1470
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```
      Lys Ser Trp Thr Ile Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro
                  270                 275                 280

      gcc cca tcc cac ttg gtg gag aag att gtc tac cac agc aag tac aag    1518
      Ala Pro Ser His Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys
                  285                 290                 295

      cca aag agg ctg ggc aat gac atc gcc ctt atg aag ctg gcc ggg cca    1566
      Pro Lys Arg Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro
                  300                 305                 310

      ctc acg ttc aat gaa atg atc cag cct gtg tgc ctg ccc aac tct gaa    1614
      Leu Thr Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu
                  315                 320                 325

      gag aac ttc ccc gat gga aaa gtg tgc tgg acg tca gga tgg ggg gcc    1662
      Glu Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala
      330                 335                 340                 345

      aca gag gat gga ggt gac gcc tcc cct gtc ctg aac cac gcg gcc gtc    1710
      Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala Val
                  350                 355                 360

      cct ttg att tcc aac aag atc tgc aac cac agg gac gtg tac ggt ggc    1758
      Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly Gly
                  365                 370                 375

      atc atc tcc ccc tcc atg ctc tgc gcg ggc tac ctg acg ggt ggc gtg    1806
      Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val
                  380                 385                 390

      gac agc tgc cag ggg gac agc ggg ggg ccc ctg gtg tgt caa gag agg    1854
      Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu Arg
                  395                 400                 405

      agg ctg tgg aag tta gtg gga gcg acc agc ttt ggc atc ggc tgc gca    1902
      Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala
      410                 415                 420                 425

      gag gtg aac aag cct ggg gtg tac acc cgt gtc acc tcc ttc ctg gac    1950
      Glu Val Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu Asp
                  430                 435                 440

      tgg atc cac gag cag atg gag aga gac cta aaa acc tgaaaaggaa          1996
      Trp Ile His Glu Gln Met Glu Arg Asp Leu Lys Thr
                  445                 450

      ggggacaagt agccacctga gttcctgagg tgatgaagac agcccgatcc tcccctggac    2056
      tcccgtgtag gaacctgcac acgagcagac acccttggag ctctgagttc cggcaccagt    2116
      agcaggcccg aaagaggcac ccttccatct gattccagca caaccttcaa gctgcttttt    2176
      gttttttgtt tttttgagat ggagtctcgc tctgttgccc aggctggagt gcagtggcga    2236
      aatccctgct cactgcagcc tccgcttccc tggttcaagc gattctcttg cctcagcttc    2296
      cccagtagct gggaccacag gtgcccgcca ccacacccaa ctaatttttg tatttttagt    2356
      agagacaggg tttcaccatg ttggccaggc tgctctcaaa cccctgacct caaatgatgt    2416
      gcctgcttca gcctcccaca gtgctgggat tacaggcatg gccaccacg cctagcctca     2476
      cgctcctttc tgatcttcac taagaacaaa agaagcagca acttgcaagg gcggcctttc    2536
      ccactggtcc atctggtttt ctctccaggg gtcttgcaaa attcctgacg agataagcag    2596
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ttatgtgacc tcacgtgcaa agccaccaac agccactcag aaaagacgca ccagcccaga   2656
agtgcagaac tgcagtcact gcacgttttc atctctaggg accagaacca aacccaccct   2716
ttctacttcc aagacttatt ttcacatgtg gggaggttaa tctaggaatg actcgtttaa   2776
ggcctatttt catgatttct ttgtagcatt tggtgcttga cgtattattg tcctttgatt   2836
ccaaataata tgtttccttc cctcatwraa maaaaaaaaa aaaaaaaarr rmrrssgcta   2896
vavmarktta gagaaaaaac ctacccacrc cttccccctg aamctraaam ya           2948
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<210> 2
<211> 453
<212> PRT
<213> Homo sapiens

<400> 2

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Met Gly Glu Asn Asp Pro Pro Ala Val Glu Ala Pro Phe Ser Phe Arg
 1               5                   10                  15
Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala Pro Asp
            20                  25                  30
Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro Leu Lys Phe
         35                  40                  45
Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile Leu Ala Leu Ala
      50                  55                  60
Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly Lys Tyr Arg Cys Arg
65                  70                  75                  80
Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala Arg Cys Asp Gly Val Ser
            85                  90                  95
Asp Cys Lys Asp Gly Glu Asp Glu Tyr Arg Cys Val Arg Val Gly Gly
            100                 105                 110
Gln Asn Ala Val Leu Gln Val Phe Thr Ala Ala Ser Trp Lys Thr Met
         115                 120                 125
Cys Ser Asp Asp Trp Lys Gly His Tyr Ala Asn Val Ala Cys Ala Gln
130                 135                 140
Leu Gly Phe Pro Ser Tyr Val Ser Ser Asp Asn Leu Arg Val Ser Ser
145                 150                 155                 160
Leu Glu Gly Gln Phe Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu
                165                 170                 175
Pro Asp Asp Lys Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu
            180                 185                 190
Gly Cys Ala Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly
         195                 200                 205
His Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu
      210                 215                 220
Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His
225                 230                 235                 240
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala Ala
                245                 250                 255
His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile Gln Val
            260                 265                 270
Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu Val Glu
         275                 280                 285
Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly Asn Asp
      290                 295                 300
Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu Met Ile
305                 310                 315                 320
Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp Gly Lys
                325                 330                 335
Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Gly Asp Ala
                340                 345                 350
```

```
Ser Pro Val Leu Asn His Ala Ala Val Pro Leu Ile Ser Asn Lys Ile
        355                 360                 365
Cys Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met Leu
    370                 375                 380
Cys Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp Ser
385                 390                 395                 400
Gly Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly
                405                 410                 415
Ala Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val
            420                 425                 430
Tyr Thr Arg Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu
        435                 440                 445
Arg Asp Leu Lys Thr
        450
```

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<210> 3
<211> 1362
<212> DNA
<213> Homo sapiens
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<400> 3
atggggaaa  atgatccgcc  tgctgttgaa  gcccccttct  cattccgatc  gcttttttggc    60
cttgatgatt  tgaaaataag  tcctgttgca  ccagatgcag  atgctgttgc  tgcacagatc   120
ctgtcactgc  tgccattgaa  gtttttttcca  atcatcgtca  ttgggatcat  tgcattgata   180
ttagcactgg  ccattggtct  gggcatccac  ttcgactgct  cagggaagta  cagatgtcgc   240
tcatccttta  agtgtatcga  gctgatagct  cgatgtgacg  gagtctcgga  ttgcaaagac   300
ggggaggacg  agtaccgctg  tgtccgggtg  ggtggtcaga  atgccgtgct  ccaggtgttc   360
acagctgctt  cgtggaagac  catgtgctcc  gatgactgga  agggtcacta  cgcaaatgtt   420
gcctgtgccc  aactgggttt  cccaagctat  gtgagttcag  ataacctcag  agtgagctcg   480
ctggagggc  agttccggga  ggagtttgtg  tccatcgatc  acctcttgcc  agatgacaag   540
gtgactgcat  acaccactc  agtatatgtg  agggagggat  gtgcctctgg  ccacgtggtt   600
accttgcagt  gcacagcctg  tggtcataga  aggggctaca  gctcacgcat  cgtgggtgga   660
aacatgtcct  tgctctcgca  gtggccctgg  caggccagcc  ttcagttcca  gggctaccac   720
ctgtgcgggg  gctctgtcat  cacgcccctg  tggatcatca  ctgctgcaca  ctgtgtttat   780
gacttgtacc  tccccaagtc  atggaccatc  caggtgggtc  tagtttccct  gttggacaat   840
ccagccccat  cccacttggt  ggagaagatt  gtctaccaca  gcaagtacaa  gccaaagagg   900
ctgggcaatg  acatcgccct  tatgaagctg  gccgggccac  tcacgttcaa  tgaaatgatc   960
cagcctgtgt  gcctgcccaa  ctctgaagag  aacttccccg  atggaaaagt  gtgctggacg  1020
tcaggatggg  gggccacaga  ggatggaggt  gacgcctccc  ctgtcctgaa  ccacgcggcc  1080
gtccctttga  tttccaacaa  gatctgcaac  cacaggacg  tgtacggtgg  catcatctcc  1140
ccctccatgc  tctgcgcggg  ctacctgacg  ggtggcgtgg  acagctgcca  ggggggacagc  1200
ggggggcccc  tggtgtgtca  agagaggagg  ctgtggaagt  tagtgggagc  gaccagcttt  1260
ggcatcggct  cgcagaggt  gaacaagcct  ggggtgtaca  cccgtgtcac  ctccttcctg  1320
gactggatcc  acgagcagat  ggagagagac  ctaaaaacct  ga                       1362
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<210> 4
<211> 260
<212> PRT
<213> Artificial Sequence
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<220>
<223> consensus sequence
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<400> 4
Ile Val Gly Gly Arg Glu Ala Gln Pro Gly Ser Phe Gly Ser Pro Trp
 1               5                  10                  15
Gln Val Ser Leu Gln Val Arg Ser Gly Gly Gly Ser Arg Lys His Phe
```

```
                    20                      25                      30
Cys Gly Gly Ser Leu Ile Ser Glu Asn Trp Val Leu Thr Ala Ala His
            35                      40                      45
Cys Val Ser Gly Ala Ala Ser Ala Pro Ala Ser Ser Val Arg Val Ser
        50                      55                      60
Leu Ser Arg Val Arg Leu Gly Glu His Asn Leu Ser Leu Thr Glu Gly
65                      70                      75                      80
Thr Glu Gln Lys Phe Asp Val Lys Lys Thr Ile Ile Val His Pro Asn
                85                      90                      95
Tyr Asn Pro Asp Thr Leu Asp Asn Gly Ala Tyr Asp Asn Asp Ile Ala
            100                     105                     110
Leu Leu Lys Leu Lys Ser Pro Gly Val Thr Leu Gly Asp Thr Val Arg
            115                     120                     125
Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp Leu Pro Val Gly Thr Thr
    130                     135                     140
Cys Thr Val Ser Gly Trp Gly Arg Arg Pro Thr Lys Asn Leu Gly Leu
145                     150                     155                     160
Ser Asp Thr Leu Gln Glu Val Val Val Pro Val Val Ser Arg Glu Thr
                165                     170                     175
Cys Arg Ser Ala Tyr Glu Tyr Gly Gly Thr Asp Asp Lys Val Glu Phe
            180                     185                     190
Val Thr Asp Asn Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala
            195                     200                     205
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Asn Arg
    210                     215                     220
Asp Gly Arg Trp Glu Leu Val Gly Ile Val Ser Trp Gly Ser Tyr Gly
225                     230                     235                     240
Cys Ala Arg Gly Asn Lys Pro Gly Val Tyr Thr Arg Val Ser Ser Tyr
            245                     250                     255
Leu Asp Trp Ile
            260


<210> 5
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 5
Arg Ile Val Gly Gly Ser Glu Ala Lys Ile Gly Ser Phe Pro Trp Gln
    1                   5                       10                      15
Val Ser Leu Gln Cys Gly Gly Ser Leu Ile Ser Pro Arg Trp Val Leu
            20                      25                      30
Thr Ala Ala His Cys Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser
            35                      40                      45
Gly Glu Glu Thr Glu Gly Gly Pro Arg Leu Asp Ser Pro Gly Gly Gln
        50                      55                      60
Val Ile Lys Val Ser Lys Ile Ile Glu Val His Pro Asn Tyr Asn Asn
65                      70                      75                      80
Asp Ile Ala Leu Leu Lys Leu Lys Glu Pro Val Thr Leu Ser Asp Ser
                85                      90                      95
Asn Thr Val Arg Pro Ile Cys Leu Pro Ser Ser Asn Glu Ile Lys Thr
            100                     105                     110
Ser Glu Gly Asn Thr Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly
        115                     120                     125
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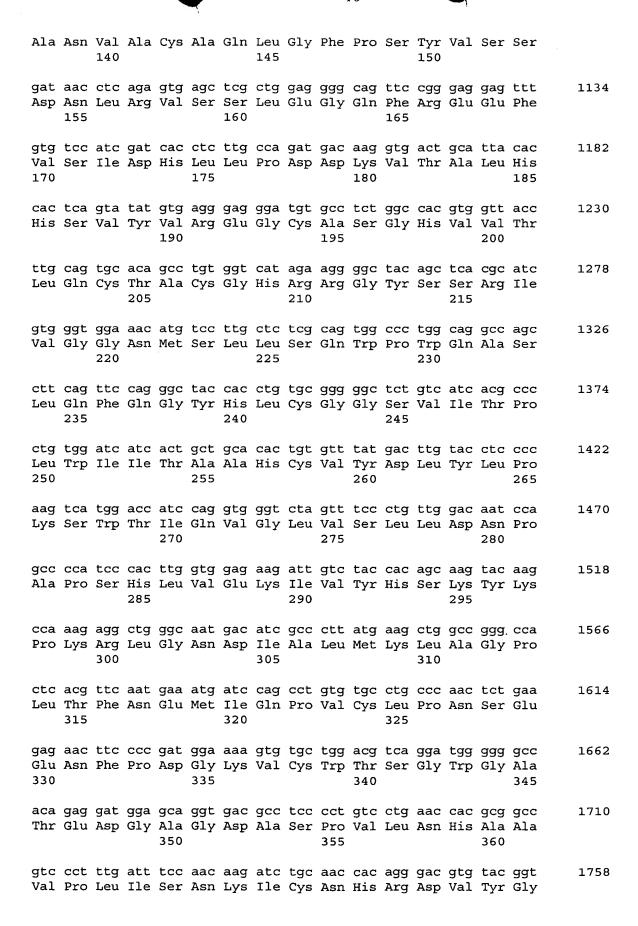
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Trp Gly Arg Thr Ser Glu Gly Pro Glu Glu Ser Gly Gly Gly Ser Leu
    130             135             140
Pro Asp Val Leu Gln Glu Val Asn Val Pro Ile Val Ser Asn Glu Thr
145             150             155             160
Cys Arg Met Leu Cys Ala Gly Tyr Leu Glu Gly Gly Asn Thr Pro Gly
            165             170             175
Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Val
            180             185             190
Leu Val Gly Ile Val Ser Trp Gly Ser Ser Ser Leu Tyr Gly Cys Ala
        195             200             205
Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser Ser Tyr Leu Asp
    210             215             220
Trp Ile
225


<210> 6
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 6
Ser Thr Cys Gly Gly Pro Asp Glu Phe Gln Cys Gly Ser Gly Arg Arg
1               5               10              15
Cys Ile Pro Arg Ser Trp Val Cys Asp Gly Asp Pro Asp Cys Glu Asp
            20              25              30
Gly Ser Asp Glu Ser Leu Glu Asn Cys Ala Ala
        35              40


<210> 7
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 7
Val Gly Gly Ser Ser Arg Cys Glu Gly Arg Val Glu Val Arg His Asp
1               5               10              15
Gly Ser Lys Trp Gly Thr Val Cys Asp Ser Ser Trp Ser Leu Arg Asp
            20              25              30
Ala Asn Val Asp Pro Gln Ala Ser Lys Val Cys Arg Gln Leu Gly Cys
            35              40              45
Gly Gly Ala Val Ser Leu Leu Gly Pro Tyr Phe Ser Glu Gly Gly Gly
    50              55              60
Pro Ala Gly Gln Arg Glu Ile Trp Leu Asp Gly Val Asn Cys Ser Gly
65              70              75              80
Asn Glu Thr Ser Leu Ser Gln Cys Pro Val Arg Val Thr Pro Pro Gly
            85              90              95
Leu Ser Arg Gln Cys Ser His Asp Gly Glu Asp Ala Gly Val Val Cys
            100             105             110
Ser
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```
<210> 8
<211> 5
<212> PRT
<213> Homo sapiens

<400> 8
Arg Ile Val Gly Gly
 1               5

<210> 9
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> motif

<221> VARIANT
<222> 2
<223> Xaa = Asp or Glu

<221> VARIANT
<222> 5
<223> Xaa = Gly or Ser

<400> 9
Gly Xaa Ser Gly Xaa
 1               5

<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> motif

<221> VARIANT
<222> 1
<223> Xaa = Leu, Ile, Val, or Met

<221> VARIANT
<222> 2
<223> Xaa = Ser or Thr

<221> VARIANT
<222> 4
<223> Xaa = Ser, Thr, Ala, or Gly

<400> 10
Xaa Xaa Ala Xaa His Cys
 1               5

<210> 11
<211> 2951
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (628)...(1989)

<221> misc_feature
<222> (1)...(2951)
<223> n = A,T,C or G

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gtatttcttc cagggtaaaa agcaaaagaa ttccggtttt ctgtatcctt ttcacttact     180
gttacccact ttgcctcgtc ttcaccctgt ccaaacaccg tctccaatt tgcccttcag      240
agaacttaag tcaaggagag ttgaaattca caggccaggg cacatctttt atttatttca     300
ttatgttggc caacagaact tgattgtaaa taataataaa gaaatctgtt atatactttc     360
caaactccaa aaaaaaccg gaattcagcc tggttaagtc caagctgaat tccgggtggg      420
ggaaggaccg ggcaccggac ggctcgggta ctttcgttct taattaggtc atgcccgtat     480
gagccaggaa agggctgtgt ttatgggaag ccagtaacac tgtggcctac tatctcttcc     540
gtggtgccat ctacattttt gggactcggg aattatgagg tagaggtgga ggcggagccg     600
gatgtcagag gtcctgaaat agtcacc atg ggg gaa aat gat ccg cct gct gtt     654
                               Met Gly Glu Asn Asp Pro Pro Ala Val
                                1               5

gaa gcc ccc ttc tca ttc cga tcg ctt ttt ggc ctt gat gat ttg aaa      702
Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys
 10              15                  20                  25

ata agt cct gtt gca cca gat gca gat gct gtt gct gca cag atc ctg      750
Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu
                30                  35                  40

tca ctg ctg cca ttg aag ttt ttt cca atc atc gtc att ggg atc att      798
Ser Leu Leu Pro Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile
                45                  50                  55

gca ttg ata tta gca ctg gcc att ggt ctg ggc atc cac ttc gac tgc      846
Ala Leu Ile Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys
                60                  65                  70

tca ggg aag tac aga tgt cgc tca tcc ttt aag tgt atc gag ctg ata      894
Ser Gly Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile
            75                  80                  85

gct cga tgt gac gga gtc tcg gat tgc aaa gac ggg gag gac gag tac      942
Ala Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr
 90                  95                  100                 105

cgc tgt gtc cgg gtg ggt ggt cag aat gcc gtg ctc cag gtg ttc aca      990
Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe Thr
                110                 115                 120

gct gct tcg tgg aag acc atg tgc tcc gat gac tgg aag ggt cac tac     1038
Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly His Tyr
                125                 130                 135

gca aat gtt gcc tgt gcc caa ctg ggt ttc cca agc tat gtg agt tca     1086
```

```
Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr Val Ser Ser
        140                 145                 150

gat aac ctc aga gtg agc tcg ctg gag ggg cag ttc cgg gag gag ttt      1134
Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe Arg Glu Glu Phe
        155                 160                 165

gtg tcc atc gat cac ctc ttg cca gat gac aag gtg act gca tta cac      1182
Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys Val Thr Ala Leu His
170                 175                 180                 185

cac tca gta tat gtg agg gag gga tgt gcc tct ggc cac gtg gtt acc      1230
His Ser Val Tyr Val Arg Glu Gly Cys Ala Ser Gly His Val Val Thr
                    190                 195                 200

ttg cag tgc aca gcc tgt ggt cat aga agg ggc tac agc tca cgc atc      1278
Leu Gln Cys Thr Ala Cys Gly His Arg Arg Gly Tyr Ser Ser Arg Ile
                205                 210                 215

gtg ggt gga aac atg tcc ttg ctc tcg cag tgg ccc tgg cag gcc agc      1326
Val Gly Gly Asn Met Ser Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser
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ctt cag ttc cag ggc tac cac ctg tgc ggg ggc tct gtc atc acg ccc      1374
Leu Gln Phe Gln Gly Tyr His Leu Cys Gly Gly Ser Val Ile Thr Pro
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ctg tgg atc atc act gct gca cac tgt gtt tat gac ttg tac ctc ccc      1422
Leu Trp Ile Ile Thr Ala Ala His Cys Val Tyr Asp Leu Tyr Leu Pro
250                 255                 260                 265

aag tca tgg acc atc cag gtg ggt cta gtt tcc ctg ttg gac aat cca      1470
Lys Ser Trp Thr Ile Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro
                    270                 275                 280

gcc cca tcc cac ttg gtg gag aag att gtc tac cac agc aag tac aag      1518
Ala Pro Ser His Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys
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cca aag agg ctg ggc aat gac atc gcc ctt atg aag ctg gcc ggg. cca      1566
Pro Lys Arg Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro
        300                 305                 310

ctc acg ttc aat gaa atg atc cag cct gtg tgc ctg ccc aac tct gaa      1614
Leu Thr Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu
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gag aac ttc ccc gat gga aaa gtg tgc tgg acg tca gga tgg ggg gcc      1662
Glu Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala
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aca gag gat gga gca ggt gac gcc tcc cct gtc ctg aac cac gcg gcc      1710
Thr Glu Asp Gly Ala Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala
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gtc cct ttg att tcc aac aag atc tgc aac cac agg gac gtg tac ggt      1758
Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly
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ggc atc atc tcc ccc tcc atg ctc tgc gcg ggc tac ctg acg ggt ggc      1806
Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly
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gtg gac agc tgc cag ggg gac agc ggg ggg ccc ctg gtg tgt caa gag      1854
Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu
        395                 400                 405

agg agg ctg tgg aag tta gtg gga gcg acc agc ttt ggc atc ggc tgc      1902
Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys
410                 415                 420                 425

gca gag gtg aac aag cct ggg gtg tac acc cgt gtc acc tcc ttc ctg      1950
Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu
                430                 435                 440

gac tgg atc cac gag cag atg gag aga gac cta aaa acc tgaagaggaa       1999
Asp Trp Ile His Glu Gln Met Glu Arg Asp Leu Lys Thr
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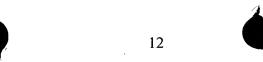
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Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro Leu Lys Phe
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Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile Leu Ala Leu Ala
    50                  55                  60
Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly Lys Tyr Arg Cys Arg
65                  70                  75                  80
Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala Arg Cys Asp Gly Val Ser
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Asp Cys Lys Asp Gly Glu Asp Glu Tyr Arg Cys Val Arg Val Gly Gly
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Gln Asn Ala Val Leu Gln Val Phe Thr Ala Ala Ser Trp Lys Thr Met
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Cys Ser Asp Asp Trp Lys Gly His Tyr Ala Asn Val Ala Cys Ala Gln
            130                 135             140
Leu Gly Phe Pro Ser Tyr Val Ser Ser Asp Asn Leu Arg Val Ser Ser
145                 150                 155                 160
Leu Glu Gly Gln Phe Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu
                165                 170                 175
Pro Asp Asp Lys Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu
                180                 185                 190
Gly Cys Ala Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly
            195                 200                 205
His Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu
            210                 215                 220
Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His
225                 230                 235                 240
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala Ala
                245                 250                 255
His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile Gln Val
                260                 265                 270
Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu Val Glu
            275                 280                 285
Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly Asn Asp
            290                 295                 300
Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu Met Ile
305                 310                 315                 320
Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp Gly Lys
                325                 330                 335
Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Ala Gly Asp
            340                 345                 350
Ala Ser Pro Val Leu Asn His Ala Ala Val Pro Leu Ile Ser Asn Lys
            355                 360                 365
Ile Cys Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met
370                 375                 380
Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp
385                 390                 395                 400
Ser Gly Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val
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Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly
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